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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/479,856DATE: 02/01/2000
TIME: 11:18:03

Input Set: I479856.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Gross, Jane A.
2 Xu, Wenfeng
3 Madden, Karen
4 Yee, David P.
5 <120> TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
6 <130> FILE REFERENCE: 98-75
7 <140> CURRENT APPLICATION NUMBER: US/09/479,856
8 <141> CURRENT FILING DATE: 2000-01-07
9 <150> EARLIER APPLICATION NUMBER: 60/115,068
10 <151> EARLIER FILING DATE: 1999-01-07
11 <150> EARLIER APPLICATION NUMBER: 60/169,890
12 <151> EARLIER FILING DATE: 1999-12-09
13 <160> NUMBER OF SEQ ID NOS: 60
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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18 <213> ORGANISM: Homo sapiens
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21 <222> LOCATION: (6)...(746)
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25 1 5 10 15
26 gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag 98
27 Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys
28 20 25 30
29 ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt 146
30 Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys
31 35 40 45
32 gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg 194
33 Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg
34 50 55 60
35 agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa 242
36 Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu
37 65 70 75
38 gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac 290
39 Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His
40 80 85 90 95
41 aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca 338
42 Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala
43 100 105 110
44 gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc 386

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45 Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala
 46 115 120 125
 47 gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg 434
 48 Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg
 49 130 135 140
 50 ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg 482
 51 Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro
 52 145 150 155
 53 gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc 530
 54 Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser
 55 160 165 170 175
 56 aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc 578
 57 Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys
 58 180 185 190
 59 agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc 626
 60 Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro
 61 195 200 205
 62 act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag 674
 63 Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln
 64 210 215 220
 65 cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722
 66 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
 67 225 230 235
 68 gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg aaaggaggag 776
 69 Ala Gln Glu Gly Pro Gly Ala
 70 240 245
 71 ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga gagagatatg 836
 72 aggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gagggagaga 896
 73 gagacagagg gagagagaga cagagggaa gagaggcaga gagggaaaga ggcagagaag 956
 74 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016
 75 gagggacaga gagagataga gcaggaggc gggcactct gagtccactt tcccacttca 1076
 76 gctgttaggtc gtcacactt aaccacacgt gcaataaaagt cctcgtgcct gctgctcaca 1136
 77 gccccggaga gccccttcctc ctggagaata aaacctttgg cagctggccct tcctca 1192
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 79 <211> LENGTH: 247
 80 <212> TYPE: PRT
 81 <213> ORGANISM: Homo sapiens
 82 <400> SEQUENCE: 2
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 84 1 5 10 15
 85 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 86 20 25 30
 87 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 88 35 40 45
 89 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 90 50 55 60
 91 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 92 65 70 75 80
 93 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 94 85 90 95

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95 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
96 100 105 110
97 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
98 115 120 125
99 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
100 130 135 140
101 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
102 145 150 155 160
103 Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
104 165 170 175
105 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg
106 180 185 190
107 Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr
108 195 200 205
109 Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro
110 210 215 220
111 Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala
112 225 230 235 240
113 Gln Glu Gly Gly Pro Gly Ala
114 245

115 <210> SEQ ID NO 3
116 <211> LENGTH: 360
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118 <213> ORGANISM: Homo sapiens
119 <220> FEATURE:
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121 <222> LOCATION: (1)...(360)
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124 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Arg Ser Arg Val Asp
125 1 5 10 15
126 cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc 96
127 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
128 20 25 30
129 tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga 144
130 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
131 35 40 45
132 cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192
133 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
134 50 55 60
135 cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240
136 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
137 65 70 75 80
138 gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288
139 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
140 85 90 95
141 ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat 336
142 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
143 100 105 110
144 cag gtg gcc ctg gtc tac agc acg 360

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RAW SEQUENCE LISTING
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Input Set: I479856.RAW

145 Gln Val Ala Leu Val Tyr Ser Thr
 146 115 120
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 148 <211> LENGTH: 120
 149 <212> TYPE: PRT
 150 <213> ORGANISM: Homo sapiens
 151 <400> SEQUENCE: 4
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 153 1 5 10 15
 154 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 155 20 25 30
 156 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 157 35 40 45
 158 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 159 50 55 60
 160 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 161 65 70 75 80
 162 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 163 85 90 95
 164 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 165 100 105 110
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 169 <211> LENGTH: 1377
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 171 <213> ORGANISM: Homo sapiens
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 173 <221> NAME/KEY: CDS
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 178 1 5 10
 179 agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97
 180 Ser Arg Val Asp Gln Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
 181 15 20 25
 182 gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145
 183 Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
 184 30 35 40
 185 ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc 193
 186 Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
 187 45 50 55 60
 188 acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc 241
 189 Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
 190 65 70 75
 191 aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
 192 Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
 193 80 85 90
 194 tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337

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RAW SEQUENCE LISTING
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Input Set: I479856.RAW

195	Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu	
196	95 100 105	
197	agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga	385
198	Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly	
199	110 115 120	
200	gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag	433
201	Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu	
202	125 130 135 140	
203	cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481
204	His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	
205	145 150 155	
206	gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529
207	Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	
208	160 165 170	
209	gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577
210	Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	
211	175 180 185	
212	agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt	625
213	Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser	
214	190 195 200	
215	ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673
216	Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val	
217	205 210 215 220	
218	agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc cct gag	721
219	Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu	
220	225 230 235	
221	tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769
222	Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp	
223	240 245 250	
224	ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817
225	Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu	
226	255 260 265	
227	cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865
228	Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val	
229	270 275 280	
230	cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa	915
231	Pro Ala Gln Glu Gly Pro Gly Ala	
232	285 290	
233	ggaggaggga gagagatgga gagaggggga gagagaaaaga gaggtgggga gaggggagag	975
234	agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag	1035
235	ggagagagag acagaggagg agagagacag aggggaagag aggcagagag gaaaagaggc	1095
236	agagaaggaa agagacaggc agagaaggag agaggcagag agggagagag gcagagaggg	1155
237	agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg	1215
238	gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtgca	1275
239	ataaagtct cgtcctgct gtcacagcc cccgagagcc ctcctcctg gagaataaaa	1335
240	ccttggcag ctgccccttcc taaaaaaaaaaa aaaaaaaaaaa aa	1377
241	<210> SEQ ID NO 6	
242	<211> LENGTH: 293	
243	<212> TYPE: PRT	
	<213> ORGANISM: Homo sapiens	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

✓

Input Set: I479856.RAW

Line ? Error/Warning

Original Text

231 W Line data has been corrected
332 W Line data has been corrected
333 W Invalid/Missing Amino Acid Numbering
490 W "N" or "Xaa" used: Feature required
492 W "N" or "Xaa" used: Feature required
494 W "N" or "Xaa" used: Feature required
508 W "N" or "Xaa" used: Feature required
509 W "N" or "Xaa" used: Feature required
510 W "N" or "Xaa" used: Feature required
511 W "N" or "Xaa" used: Feature required
512 W "N" or "Xaa" used: Feature required
513 W "N" or "Xaa" used: Feature required
526 W "N" or "Xaa" used: Feature required
527 W "N" or "Xaa" used: Feature required
528 W "N" or "Xaa" used: Feature required
529 W "N" or "Xaa" used: Feature required
530 W "N" or "Xaa" used: Feature required
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532 W "N" or "Xaa" used: Feature required
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534 W "N" or "Xaa" used: Feature required
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537 W "N" or "Xaa" used: Feature required
538 W "N" or "Xaa" used: Feature required
738 W Invalid/Missing Amino Acid Numbering

Pro Ala Gln Glu Gly Gly Pro Gly Ala *
Ala Arg *

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Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa X
Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa
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athwsntgyg cnwsnathtg yggncarcay ccnaarca
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athwsntgyg cnwsnathtg yggncarcay ccnaarca
aarytnmgnw snccngtnaa yytncnccn garytnmng
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aaraarmgng gngayccntg ywsntgycar ccnmgnws
aarwsnwsnc argaycaygc natggargcn ggnwsncc
gtngaracnt gywsnttgyt yttycngar tgymgnngc
acnccnggna cnccngaycc nacntgygcn ggnmgnngt
gtnytnarc cntgycnca yathccngay wsnggnyt
cargargng gnccnggngc n

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CORRECTION SUMMARY
PATENT APPLICATION US/09/479,856

DATE: 02/01/2000

TIME: 11:18:03

Input Set: **I479856.RAW**

Line Original Text

Corrected Data

231 Pro Ala Gln Glu Gly Gly Pro Gly Ala * Pro Ala Gln Glu Gly Gly Pro Gly Ala
332 Ala Arg * Ala Arg